

PRIMER G →

1 aaacaagataaaaacatgattatcaacatTTTTactTTTccactttctgtggaa  
1-----+-----+-----+-----+-----+-----+-----+60

61 aactttattaaaatatccacttacccattatTTTTtagattatccacaaaaatgtgga  
61-----+-----+-----+-----+-----+-----+-----+120

121 <sup>-35</sup> gaaactatattatTTGATTttgttactattaaggTATTtaagtgagagtagatata  
121-----+-----+-----+-----+-----+-----+-----+180

181 <sup>-10</sup> <sup>-10</sup> <sup>-10</sup>  
RBS  
attacatcatagaaatgctacaaagattaataattgaaaggattattatgcaaaaagc  
181-----+-----+-----+-----+-----+-----+-----+-----+240  
M A K A

PRIMER F →

241 taatataggaaaattgctattaacaggtgtcggtggcgagccatcgacttggaggaag  
241-----+-----+-----+-----+-----+-----+-----+-----+300  
N I G K L L L T G V V G G A I A L G G S

TRANSMEMBRANE DOMAINE

301 tgcaatctatcaaaggactacaaatcaatcgccaaataatagtcgttcaaataactag  
301-----+-----+-----+-----+-----+-----+-----+-----+360  
A I Y Q S T T N Q S A N N N S R S N T T S

361 tacaaggtagtaacgtttcgtaatgtcaataccgatgttacctctgcaattgaaaa  
361-----+-----+-----+-----+-----+-----+-----+-----+420  
T K V S N V S V N V N T D V T S A I E K

421 agttcaattctgtcgttctgttatgaattatcaaaaagataactcacaaggtagtga  
421-----+-----+-----+-----+-----+-----+-----+-----+480  
V S N S V V S V M N Y Q K D N S Q S S D

481 cttcagttcaattttgggtggaaatagcggttcaagttcatcgactgatggcttacagct  
481-----+-----+-----+-----+-----+-----+-----+-----+540  
F S S I F G G N S G S S S S T D G L Q L

541 ttctagtgaaggctctgggtcatctacaaaaatctgggtgatgcctacgtttaac  
541-----+-----+-----+-----+-----+-----+-----+-----+600  
S S E G S G V I Y K K S G G D A Y V V T

CATALYTIC DOMAINE

601 taactaccacgttattgtggtaatagctactgtatgttctgtttctgggacaaaa  
601-----+-----+-----+-----+-----+-----+-----+-----+660  
N Y H V I A G N S S L D V L L S G G Q K

**FIG. 1**

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661 agtcaaagattctgtgggttatgatgaatacacagacccgtgttctaaaatcag  
 661-----+-----+-----+-----+-----+-----+-----+-----+720  
 V K D S V V G Y D E Y T **D** L **A** **V** L K I S  
 CATALYTIC DOMAINE  
 721 ttctgaacatgtcaaagatgtggcgacattcgctgattcttagtaaattaacaattggtaa  
 721-----+-----+-----+-----+-----+-----+-----+-----+780  
 S E H V K D V A T F A D S S K L T I G E  
 781 acctgccattgccgttggctcacctttaggttagtcaatttgcacacccgcaactgaagg  
 781-----+-----+-----+-----+-----+-----+-----+-----+840  
 P A I A V G S P L G S Q F A N T A T E G  
 841 aattttatctgcaacaaggccgtcaagtgactttgacccaagaaaaatggtcaaacaactaa  
 841-----+-----+-----+-----+-----+-----+-----+-----+900  
 I L S A T S R Q V T L T Q E N G Q T T N  
 ←PRIMER A  
 901 tatcaatgcaattcaaacagatgctgccattaaccctggtaactctggaggggcttgat  
 901-----+-----+-----+-----+-----+-----+-----+-----+960  
 I N A I Q T D A A I N P **G** **N** **S** **G** **G** A **L** I  
 CATALYTIC DOMAINE  
 961 taatattgaaggacaagttattgaaattactcaaagtaaaattacaacaactgaagatgg  
 961-----+-----+-----+-----+-----+-----+-----+-----+1020  
**N** I E **G** Q V **I** **G** **I** T Q S K I T T T E D G  
 1021 ttctacttctgtcgaagggttaggattgcgattccttcaatgatgtcgtaaatatcat  
 1021-----+-----+-----+-----+-----+-----+-----+-----+1080  
 S T S V E G L G F A I P S N D V V N I I  
 1081 taataaactgaagatgatgtaagattcacgcctgcttaggtatccgaatggtaa  
 1081-----+-----+-----+-----+-----+-----+-----+-----+1140  
 N K L E D D G K I S R P A L G I R M V D  
 1141 ccttcacaattatcaacaaatgacagttctcaattgaaattactaaggcagtgtacagg  
 1141-----+-----+-----+-----+-----+-----+-----+-----+1200  
 L S Q L S T N D S S Q L K L L S S V T G  
 1201 tggggttgttactccgtccatctggacttcctgctgcctcagctggttgaaagc  
 1201-----+-----+-----+-----+-----+-----+-----+-----+1260  
 G V V V Y S V Q S G L P A A S A G L K A  
 1261 tggagatgtaattacaaagggtggcgatacagcagtaacctcttcaacagacttgcaaag  
 1261-----+-----+-----+-----+-----+-----+-----+-----+1320  
 G D V I T K V G D T A V T S S T D L Q S

**FIG. 1**  
(CONTINUED)

1321 tgctcttactcacacaatcaatgatacagtaaaagttaacttattatcgatggtaa 1380  
A L Y S H N I N D T V K V T Y Y R D G K

1381 atcaaatacagcagatgttaacttctaaatcaaccagtgacttagaaacaaggcgtcc 1440  
S N T A D V K L S K S T S D L E T S S P

1441 atcttcttcaatt**taataacttaataatttaataaaaagtcttctgtaaatagaaggctt** 1500  
S S S N

1501 tttcataactaaagtctgaaattttaaaaataataaaattccattttctttattgatt 1560

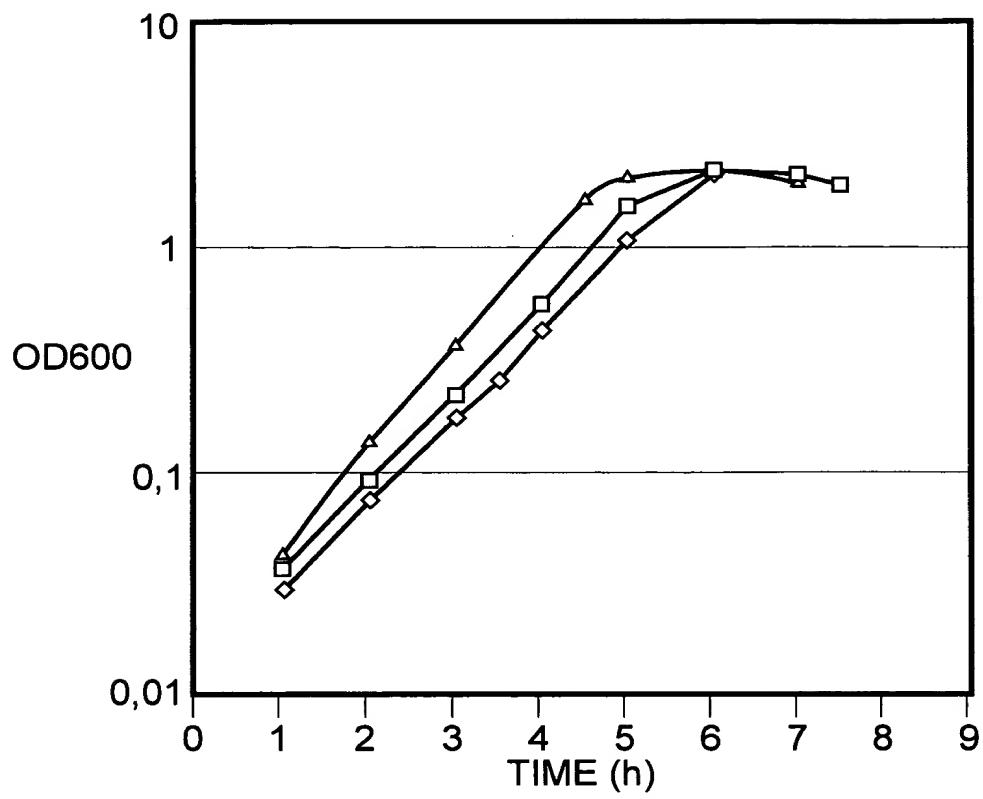
1561 **tatggtaaaataaagttaagcatgaaaatttactttacttagaagccgaacaattttg** 1620

1621 agtcattcaggaattggtcgtcaatgaaacatcaacaacgcgccttgatttaatggc 1680

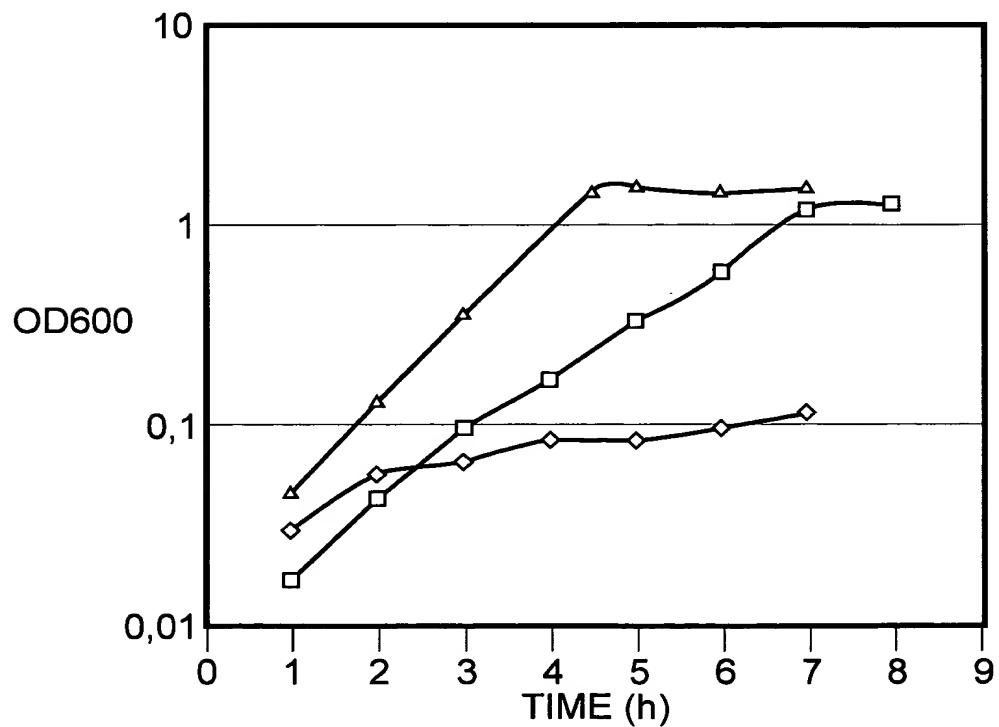
1681 attgactggacaaaaatcctgaggatgattacgatattccattaaatacttatggc 1740

**FIG. 1**  
**(CONTINUED)**

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**FIG. 2A**



**FIG. 2B**

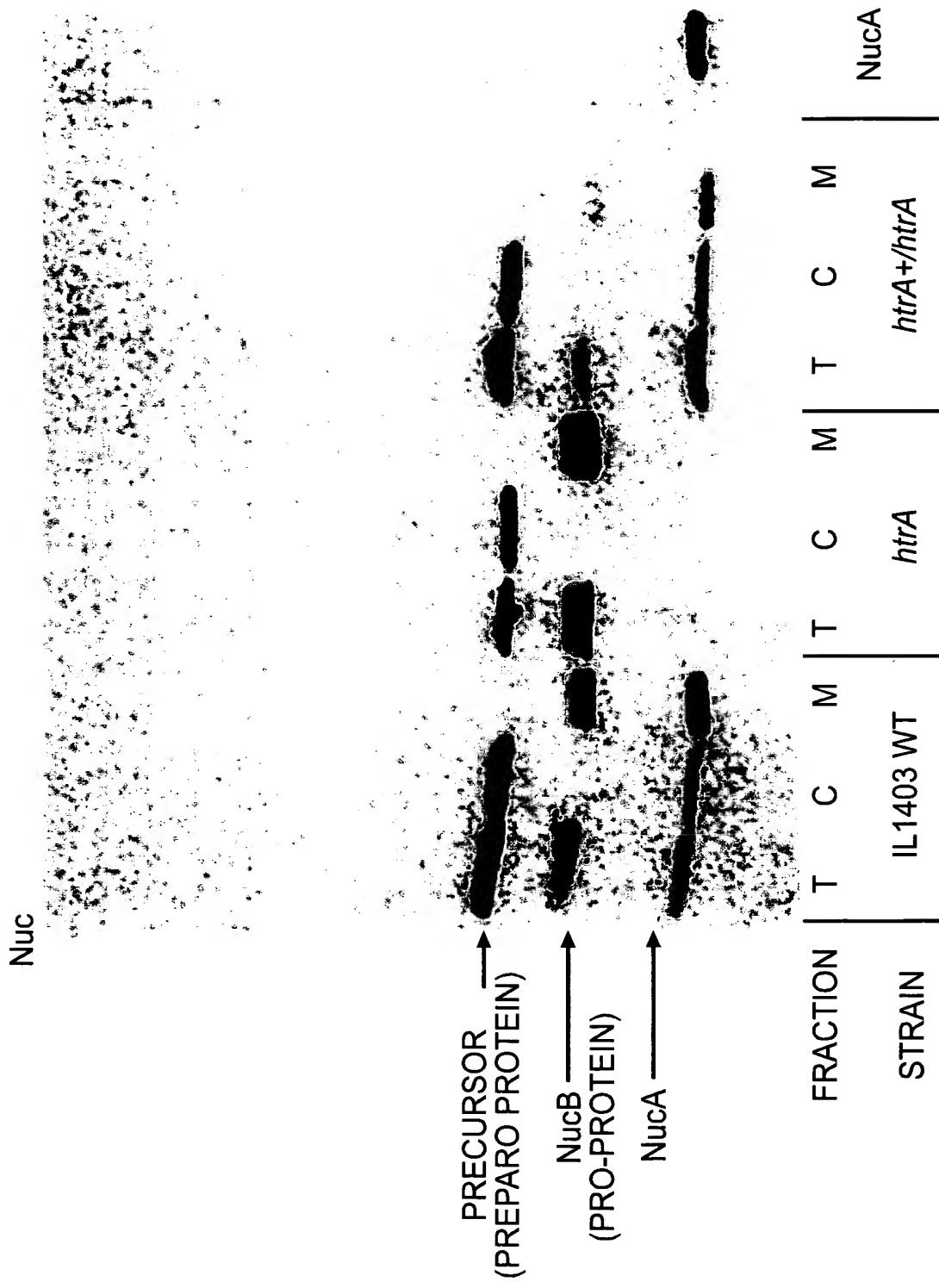


FIG. 3

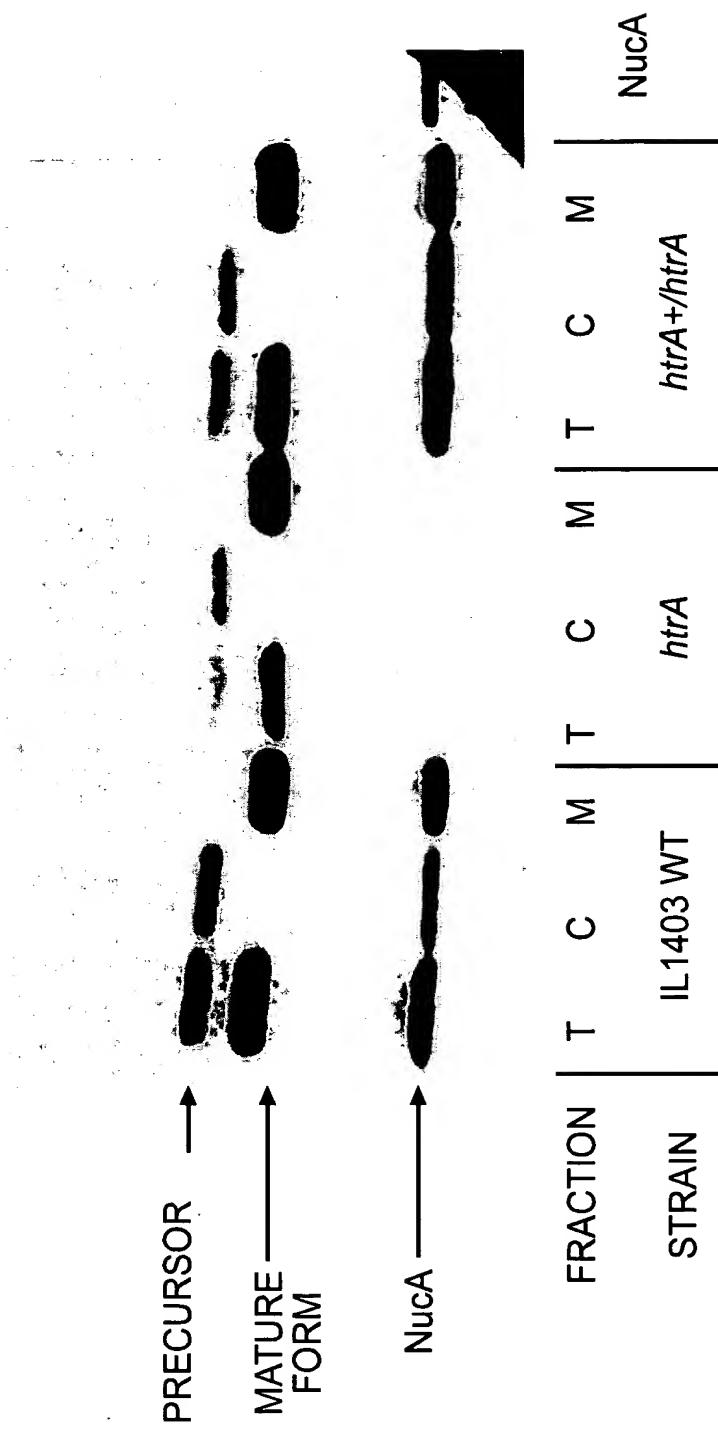
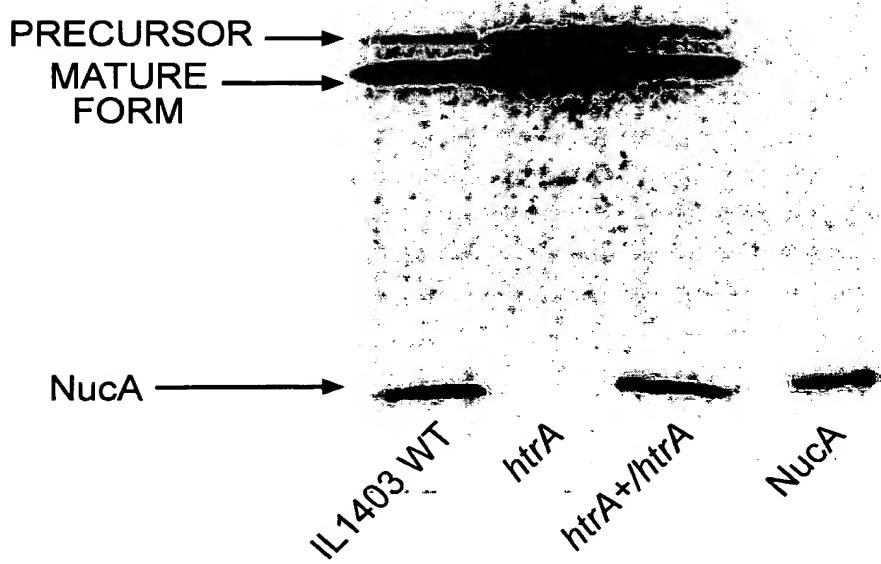
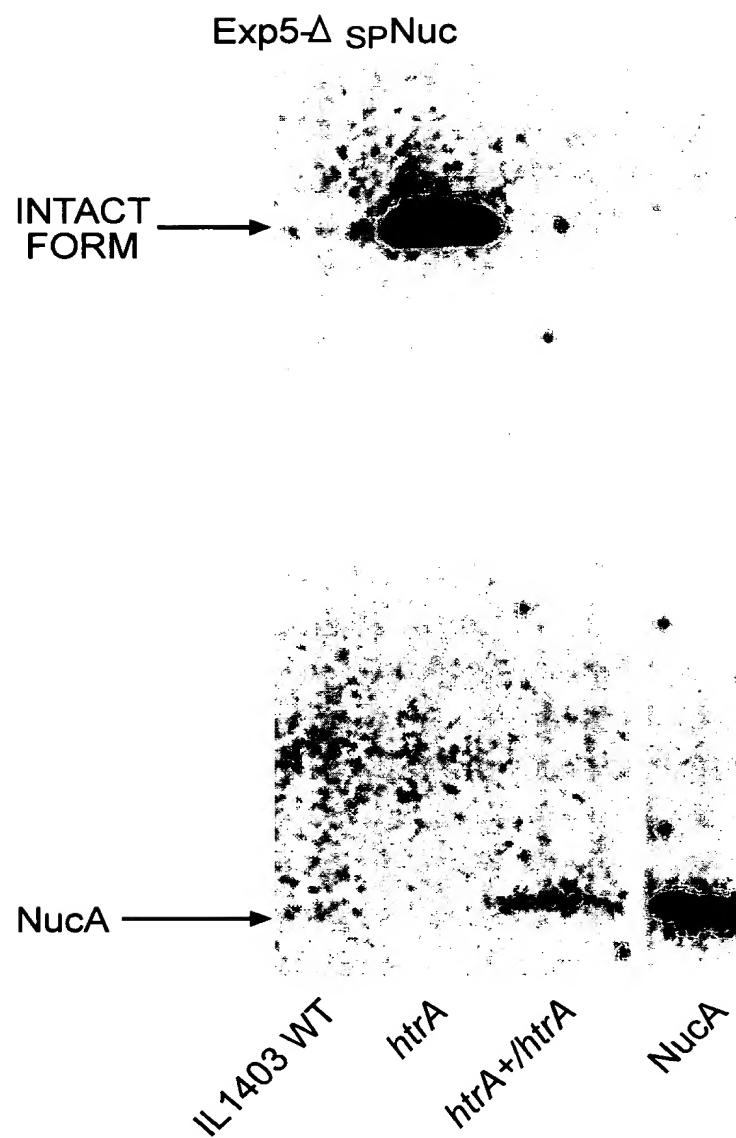
Usp- $\Delta$ SPNuc

FIG. 4

Nlp4- $\Delta$ SPNuc

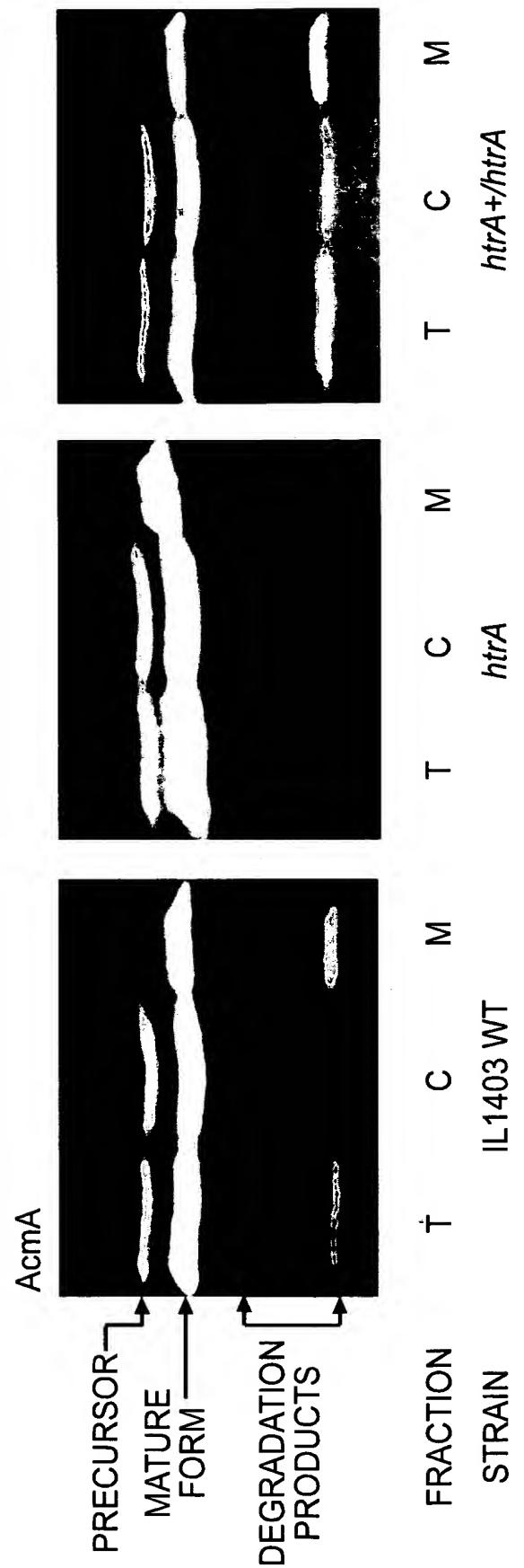


**FIG. 5**



**FIG. 6**

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**FIG. 7**

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